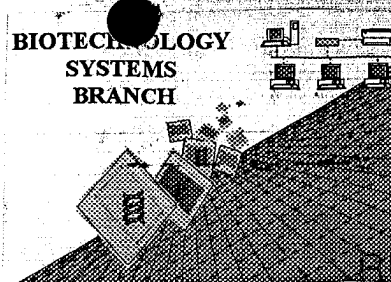


*P. Ben*

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



RECEIVED

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form: DEC 14 2000

TECH CENTER 1600/2900

Application Serial Number: 09/284,697

Source: 1638

Date Processed by STIC: 12/1/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/284,697

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid-number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

P. BUI

#106  
12/19/00  
1638

**IMPORTANT:** see item 5 on  
Erra summary sheet  
Does Not Comply  
Corrected Diskette Needed

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/284,697

DATE: 12/01/2000  
TIME: 08:23:23

Input Set : A:\ES.txt  
Output Set: N:\CRF3\12012000\I284697.raw

3 <110> APPLICANT: MERTSTEM THERAPEUTICS S.A.  
5 <120> TITLE OF INVENTION: Pancreatic Lipases and/or Recombinant Colipases and  
6 Derived Polypeptides Produced by Plants, Methods for  
7 Obtaining Them and UseThereof.  
9 <130> FILE REFERENCE: 1074-1168PCT-US octobre 2000  
11 <140> CURRENT APPLICATION NUMBER: US 09/284,697  
12 <141> CURRENT FILING DATE: 1999-07-06  
14 <150> PRIOR APPLICATION NUMBER: PCT/FR97/01862  
15 <151> PRIOR FILING DATE: 1997-10-17  
17 <160> NUMBER OF SEQ ID NOS: 16  
19 <170> SOFTWARE: PatentIn Ver. 2.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 69  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Artificial Sequence  
26 <220> FEATURE:  
27 <223> OTHER INFORMATION: Description of Artificial Sequence: signal peptide  
29 <220> FEATURE:  
30 <221> NAME/KEY: misc\_feature  
31 <222> LOCATION: (1)..(69)  
32 <223> OTHER INFORMATION: Signal peptide of Sporamine A of Sweet potato  
34 <220> FEATURE:  
35 <221> NAME/KEY: CDS  
36 <222> LOCATION: (1)..(69)  
38 <300> PUBLICATION INFORMATION:  
39 <303> JOURNAL: J. Biol. Chem.  
40 <304> VOLUME: 264  
41 <306> PAGES: 20042-20048  
42 <307> DATE: 1989  
44 <400> SEQUENCE: 1  
45 atg aaa gcc ttc aca ctc gct ctc ttc tta gct ctt tcc ctc tat ctc 48  
46 Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu  
47 1 5 10 15  
49 ctg ccc aat cca gcc cat tcc 69  
50 Leu Pro Asn Pro Ala His Ser  
51 20  
54 <210> SEQ ID NO: 2  
55 <211> LENGTH: 23  
56 <212> TYPE: PRT  
57 <213> ORGANISM: Artificial Sequence  
W--> 58 <220> FEATURE: Insert this mandatory numeric identifier whenever  
58 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide  
60 <400> SEQUENCE: 2  
61 Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu  
62 1 5 10 15  
64 Leu Pro Asn Pro Ala His Ser  
65 20

Sequence 1 is a nucleotide sequence.

It should be a sufficient  
Explanation for (213) Artificial  
Sequence.

↓  
give  
source  
of genetic  
material  
C2217, C2227, or  
C2237 is  
short

see circled portion of item 12  
on Erra summary sheet

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/284,697

DATE: 12/01/2000  
TIME: 08:23:23

Input Set : A:\ES.txt  
Output Set: N:\CRF3\12012000\I284697.raw

69 <210> SEQ ID NO: 3  
70 <211> LENGTH: 111  
71 <212> TYPE: DNA  
72 <213> ORGANISM: Artificial Sequence  
74 <220> FEATURE:  
75 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide  
77 <220> FEATURE:  
78 <221> NAME/KEY: sig\_peptide  
79 <222> LOCATION: (1)..(111)  
80 <223> OTHER INFORMATION: Signal peptide PPS of Sporamine A of Sweet potato.  
82 <220> FEATURE:  
83 <221> NAME/KEY: CDS  
84 <222> LOCATION: (1)..(111)  
86 <300> PUBLICATION INFORMATION:  
87 <303> JOURNAL: J. Biol. Chem.  
88 <304> VOLUME: 264  
89 <306> PAGES: 20042-20048  
90 <307> DATE: 1989  
92 <400> SEQUENCE: 3  
93 atg aaa gcc ttc aca ctc gct ctc ttc tta gct ctt tcc ctc tat ctc 48  
94 Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu  
95 1 5 10 15  
97 ctg ccc aat cca gcc cat tcc agg ttc aat ccc atc cgc ctc ccc acc 96  
98 Leu Pro Asn Pro Ala His Ser Arg Phe Asn Pro Ile Arg Leu Pro Thr  
99 20 25 30  
101 aca cac gaa ccc gcc 111  
102 Thr His Glu Pro Ala  
103 35

106 <210> SEQ ID NO: 4  
107 <211> LENGTH: 37  
108 <212> TYPE: PRT  
109 <213> ORGANISM: Artificial Sequence  
110 <220> FEATURE: insert  
110 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide give source  
112 <400> SEQUENCE: 4  
113 Met Lys Ala Phe Thr Leu Ala Leu Phe Leu Ala Leu Ser Leu Tyr Leu  
114 1 5 10 15  
116 Leu Pro Asn Pro Ala His Ser Arg Phe Asn Pro Ile Arg Leu Pro Thr  
117 20 25 30  
119 Thr His Glu Pro Ala  
120 35  
124 <210> SEQ ID NO: 5  
125 <211> LENGTH: 66  
126 <212> TYPE: DNA  
127 <213> ORGANISM: Artificial Sequence  
129 <220> FEATURE:  
130 <223> OTHER INFORMATION: Description of Artificial Sequence: Signal peptide  
132 <220> FEATURE:  
133 <221> NAME/KEY: sig\_peptide

*Seq 3 is a nucleotide sequence*

Signal peptide

Sweet

OK

W-->

*Sequence 5 is a nucleotide sequence*

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/284,697  
 DATE: 12/01/2000  
 TIME: 08:23:23

Input Set : A:\ES.txt  
 Output Set: N:\CRF3\12012000\I284697.raw

134 <222> LOCATION: (1)..(66)  
 135 <223> OTHER INFORMATION: Signal peptide of rappbit gastric lipase  
 137 <220> FEATURE:  
 138 <221> NAME/KEY: CDS  
 139 <222> LOCATION: (1)..(66)  
 141 <400> SEQUENCE: 5  
 142 atg tgg gtg ctt ttc atg gtg gca gct tlg cta tct gca ctt gga act 48  
 143 Met Trp Val Leu Phe Met Val Ala Ala Leu Leu Ser Ala Leu Gly Thr  
 144 1 5 10 15 66  
 146 aca cat ggt ctt ttt gga  
 147 Thr His Gly Leu Phe Gly  
 148 20  
 151 <210> SEQ ID NO: 6  
 152 <211> LENGTH: 22  
 153 <212> TYPE: PRT  
 154 <213> ORGANISM: Artificial Sequence  
 W--> 155 <220> FEATURE: *insert*  
 155 <223> OTHER INFORMATION: Description of Artificial Sequence Signal peptide *give source*  
 157 <400> SEQUENCE: 6  
 158 Met Trp Val Leu Phe Met Val Ala Ala Leu Leu Ser Ala Leu Gly Thr  
 159 1 5 10 15  
 161 Thr His Gly Leu Phe Gly  
 162 20  
 166 <210> SEQ ID NO: 7  
 167 <211> LENGTH: 48  
 168 <212> TYPE: DNA  
 169 <213> ORGANISM: Artificial Sequence  
 171 <220> FEATURE:  
 172 <223> OTHER INFORMATION: Description of Artificial Sequence Signal peptide  
 174 <220> FEATURE:  
 175 <221> NAME/KEY: sig\_peptide  
 176 <222> LOCATION: (1)..(48)  
 177 <223> OTHER INFORMATION: Signal peptide of PSHPL.  
 179 <220> FEATURE:  
 180 <221> NAME/KEY: CDS  
 181 <222> LOCATION: (1)..(48)  
 182 <223> OTHER INFORMATION: The cleavage sequence between the two sequences  
 183 coding for PSPHPL and HPL is Gly-Lys.  
 185 <400> SEQUENCE: 7  
 186 atg ctg cca ctt tgg act ctt tca ctg ctg ctg gga gca gta gca gga 48  
 187 Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Leu Gly Ala Val Ala Gly  
 188 1 5 10 15  
 191 <210> SEQ ID NO: 8  
 192 <211> LENGTH: 16  
 193 <212> TYPE: PRT  
 194 <213> ORGANISM: Artificial Sequence  
 W--> 195 <220> FEATURE: *insert*  
 195 <223> OTHER INFORMATION: Description of Artificial Sequence Signal peptide *give source*  
 197 <400> SEQUENCE: 8

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/284,697

DATE: 12/01/2000

TIME: 08:23:23

Input Set : A:\ES.txt

Output Set: N:\CRF3\12012000\I284697.raw

198 Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Gly Ala Val Ala Gly  
 199 1 5 10 15

203 &lt;210&gt; SEQ ID NO: 9

204 &lt;211&gt; LENGTH: 66

205 &lt;212&gt; TYPE: DNA

206 &lt;213&gt; ORGANISM: Artificial Sequence

208 &lt;220&gt; FEATURE:

209 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Signal peptide

211 &lt;220&gt; FEATURE:

212 &lt;221&gt; NAME/KEY: sig\_peptide

213 &lt;222&gt; LOCATION: (1)..(66)

214 &lt;223&gt; OTHER INFORMATION: Signal peptide of HPCOL

216 &lt;220&gt; FEATURE:

217 &lt;221&gt; NAME/KEY: CDS

218 &lt;222&gt; LOCATION: (1)..(66)

220 &lt;400&gt; SEQUENCE: 9

221 atg tgg gtc ctt ttc atg gtc gca gct ttg cta tct gca ctt gga act 48

222 Met Trp Val Leu Phe Met Val Ala Ala Leu Leu Ser Ala Leu Gly Thr

223 1 5 10 15

225 aca cat ggt ctt ttt gga 66

226 Thr His Gly Leu Phe Gly

227 20

230 &lt;210&gt; SEQ ID NO: 10

231 &lt;211&gt; LENGTH: 22

232 &lt;212&gt; TYPE: PRT

233 &lt;213&gt; ORGANISM: Artificial Sequence

W--&gt; 234 &lt;220&gt; FEATURE:

234 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Signal peptide

236 &lt;400&gt; SEQUENCE: 10

237 Met Trp Val Leu Phe Met Val Ala Ala Leu Leu Ser Ala Leu Gly Thr

238 1 5 10 15

240 Thr His Gly Leu Phe Gly

241 20

245 &lt;210&gt; SEQ ID NO: 11

246 &lt;211&gt; LENGTH: 51

247 &lt;212&gt; TYPE: DNA

248 &lt;213&gt; ORGANISM: Artificial Sequence

250 &lt;220&gt; FEATURE:

251 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Signal peptide

253 &lt;220&gt; FEATURE:

254 &lt;221&gt; NAME/KEY: sig\_peptide

255 &lt;222&gt; LOCATION: (1)..(51)

256 &lt;223&gt; OTHER INFORMATION: Signal peptide of PSHPOL.

258 &lt;220&gt; FEATURE:

259 &lt;221&gt; NAME/KEY: CDS

260 &lt;222&gt; LOCATION: (1)..(51)

261 &lt;223&gt; OTHER INFORMATION: The cleavage sequence between the two sequences

262 coding for PSHPOL and HPCOL is Ala-Lys.

264 &lt;400&gt; SEQUENCE: 11

*nucleotide sequence**insert**gene source**nucleotide sequence*

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/284,697  
 DATE: 12/01/2000  
 TIME: 08:23:23

Input Set : A:\ES.txt  
 Output Set: N:\CRF3\12012000\I284697.raw

RECEIVED

DEC 14 2000

TECH CENTER 1600/2900

265 atg gag aag atc ctg atc ctc ctg ctt gtc gcc ctc tct gtg gcc tat 48  
 266 Met Glu Lys Ile Leu Ile Leu Leu Val Ala Leu Ser Val Ala Tyr  
 267 1 5 10 15  
 269 gca 51  
 270 Ala  
 273 <210> SEQ ID NO: 12  
 274 <211> LENGTH: 17  
 275 <212> TYPE: PRT  
 276 <213> ORGANISM: Artificial Sequence  
 W--> 277 <220> FEATURE: *insert*  
 277 <223> OTHER INFORMATION: Description of Artificial Sequence Signal peptide  
 279 <400> SEQUENCE: 12  
 280 Met Glu Lys Ile Leu Ile Leu Leu Val Ala Leu Ser Val Ala Tyr  
 281 1 5 10 15  
 283 Ala  
 288 <210> SEQ ID NO: 13  
 289 <211> LENGTH: 32  
 290 <212> TYPE: DNA  
 291 <213> ORGANISM: Artificial Sequence  
 293 <220> FEATURE:  
 294 <223> OTHER INFORMATION: Description of Artificial  
 295 Sequence: oligodeoxynucleotide  
 297 <220> FEATURE:  
 298 <221> NAME/KEY: misc\_feature  
 299 <222> LOCATION: (1)..(32)  
 300 <223> OTHER INFORMATION: Oligodeoxynucleotide used to construct the adapter  
 301 carrying restriction sites PacI, AscI, MluI and  
 302 HpaI.  
 304 <400> SEQUENCE: 13  
 305 agotgattaa ttaaggcgcg ccacgcgtta ac 32  
 308 <210> SEQ ID NO: 14  
 309 <211> LENGTH: 32  
 310 <212> TYPE: DNA  
 311 <213> ORGANISM: Artificial Sequence  
 313 <220> FEATURE:  
 314 <223> OTHER INFORMATION: Description of Artificial  
 315 Sequence: oligodeoxynucleotide  
 317 <220> FEATURE:  
 318 <221> NAME/KEY: misc\_feature  
 319 <222> LOCATION: (1)..(32)  
 320 <223> OTHER INFORMATION: Oligodeoxynucleotide used to construct the adapter  
 321 carrying the restriction sites PacI, AscI, MluI  
 322 and HpaI.  
 324 <400> SEQUENCE: 14  
 325 aattgttaac gcgtggcgcg cottaattaa tc 32  
 328 <210> SEQ ID NO: 15  
 329 <211> LENGTH: 523  
 330 <212> TYPE: DNA  
 331 <213> ORGANISM: Homo sapiens

*give name*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/284,697

DATE: 12/01/2000

TIME: 08:23:24

Input Set : A:\ES.txt

Output Set: N:\CRF3\12012000\I284697.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:42 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
 L:58 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:90 M:285 W: Invalid Journal Date: Wrong YYYY-MM-DD,MMM-YYYY or SEASON-YYYY, Wrong Journal Date:YYYY-MM-DD,MMM-YYYY or Season-YYYY  
 L:110 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:155 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:195 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:234 M:258 W: Mandatory Feature missing, <220> FEATURE:  
 L:277 M:258 W: Mandatory Feature missing, <220> FEATURE: